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<a href="#">#8</a>	Search eptiope AND repeat AND ( <b>plasmodium or falciparum</b> ) AND ("liver stage" or liver-stage or LSA*)	09:53:02	<a href="#">0</a>
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<input type="checkbox"/>	L8	L6 and (@ad<19910205 or @pd<19920205)	1
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<input type="checkbox"/>	L6	(t adj (cell or lymphocyte) or cellular) with Epitope and (LSA\$2 or (liver-stage or liver adj stage) adj3 (protein or antigen)) with (malaria or plasmodium or falciparum)	124
<input type="checkbox"/>	L5	(malaria or plasmodium or falciparum) same(immunoassay or (detect\$ or determin\$) with (antibod\$6 or immunoglob\$9))	543
<input type="checkbox"/>	L4	L1 and (@ad<19910205 or @pd<19920205)	85
<input type="checkbox"/>	L3	L1 and fusion same (epitop\$3 or peptides)	206
<input type="checkbox"/>	L2	(malaria or plasmodium or falciparum) same(immunoassay or (detect\$ or determin\$) with (antibod\$6 or immunoglob\$9))	543
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BLASTN 2.2.14 [May-07-2006]

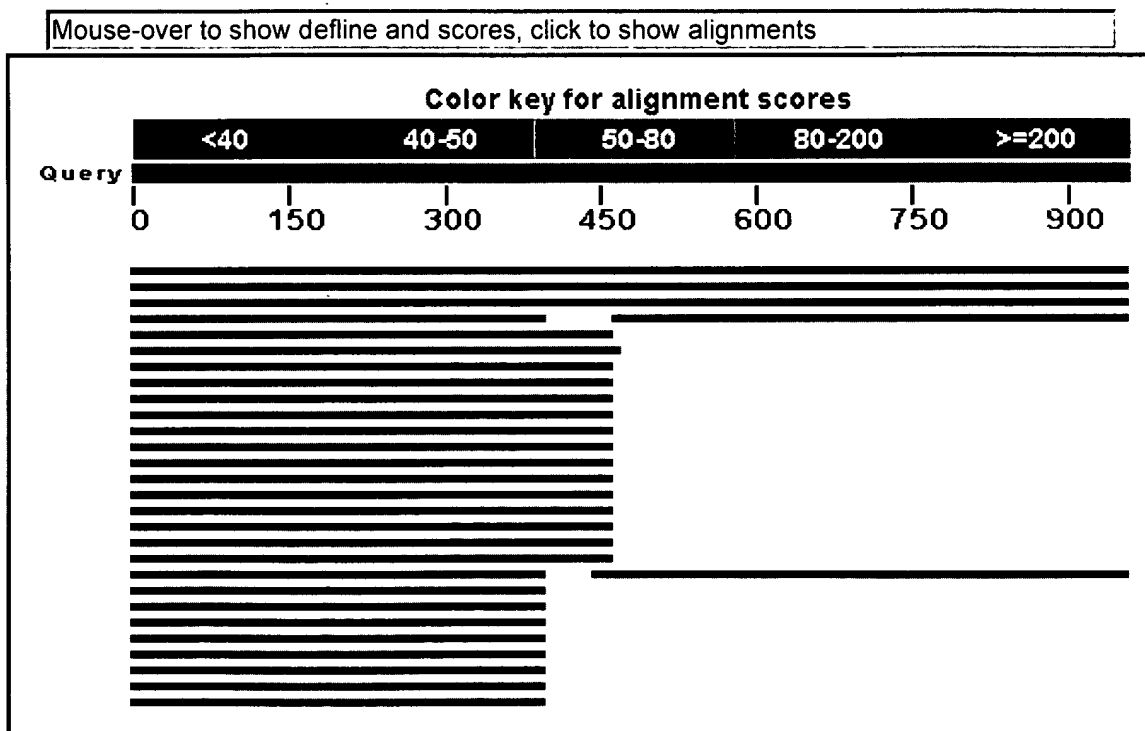
RID: 1158783042-7538-80683885490.BLASTQ4

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
4,365,567 sequences; 18,294,867,195 total letters

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Query= *SEQ 10 NO. 38*  
Length=954

## Distribution of 184 Blast Hits on the Query Sequence



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Sequences producing significant alignments:		Score (Bits)	E Value
<a href="#">gi 510185 emb Z30319.1 PFLSA15</a>	P.falciparum LSA-1 gene for liver	1729	0.0
<a href="#">gi 9915 emb X56203.1 PFLSA1G</a>	P.falciparum LSA-1 gene for liver s	1635	0.0
<a href="#">gi 23495173 gb AE014834.1 </a>	Plasmodium falciparum 3D7 chromoso...	1526	0.0
<a href="#">gi 510183 emb Z30320.1 PFLSA13</a>	P.falciparum LSA-1 gene for liver	821	0.0
<a href="#">gi 950655 gb L40911.1 PFALSA1D</a>	Plasmodium falciparum (clones ...	815	0.0
<a href="#">gi 1435204 gb U60974.1 PFU60974</a>	Plasmodium falciparum liver s...	811	0.0
<a href="#">gi 725321 gb L40942.1 PFALSA1P</a>	Plasmodium falciparum (clone K...	809	0.0
<a href="#">gi 725319 gb L40941.1 PFALSA1O</a>	Plasmodium falciparum (clones ...	809	0.0

<a href="#">gi 725311 gb L40946.1 PFALSA1K</a>	Plasmodium falciparum (clone B...	809	0.0
<a href="#">gi 950658 gb L40914.1 PFALSA1H</a>	Plasmodium falciparum (clone K...	809	0.0
<a href="#">gi 950656 gb L40912.1 PFALSA1E</a>	Plasmodium falciparum (clone K...	809	0.0
<a href="#">gi 725325 gb L40944.1 PFALSA1R</a>	Plasmodium falciparum (clones ...	804	0.0
<a href="#">gi 725323 gb L40943.1 PFALSA1Q</a>	Plasmodium falciparum (clones ...	804	0.0
<a href="#">gi 950657 gb L40913.1 PFALSA1F</a>	Plasmodium falciparum (clone K...	804	0.0
<a href="#">gi 950661 gb L40922.1 PFALSA1L</a>	Plasmodium falciparum (clone K...	798	0.0
<a href="#">gi 950660 gb L40918.1 PFALSA1J</a>	Plasmodium falciparum (clone K...	798	0.0
<a href="#">gi 950659 gb L40917.1 PFALSA1I</a>	Plasmodium falciparum (clone K...	787	0.0
<a href="#">gi 950662 gb L40923.1 PFALSA1M</a>	Plasmodium falciparum (clone K...	782	0.0
<a href="#">gi 725291 gb L40945.1 PFALSA1</a>	Plasmodium falciparum (clone BR...	776	0.0
<a href="#">gi 3643906 gb AF086796.1 AF086796</a>	Plasmodium falciparum strai...	723	0.0
<a href="#">gi 3643900 gb AF086793.1 AF086793</a>	Plasmodium falciparum strai...	723	0.0
<a href="#">gi 3643918 gb AF086802.1 AF086802</a>	Plasmodium falciparum strai...	712	0.0
<a href="#">gi 3643912 gb AF086799.1 AF086799</a>	Plasmodium falciparum strai...	712	0.0
<a href="#">gi 3643910 gb AF086798.1 AF086798</a>	Plasmodium falciparum strai...	712	0.0
<a href="#">gi 3643916 gb AF086801.1 AF086801</a>	Plasmodium falciparum strai...	706	0.0
<a href="#">gi 3643914 gb AF086800.1 AF086800</a>	Plasmodium falciparum strai...	706	0.0
<a href="#">gi 3643908 gb AF086797.1 AF086797</a>	Plasmodium falciparum strai...	706	0.0
<a href="#">gi 3643904 gb AF086795.1 AF086795</a>	Plasmodium falciparum strai...	706	0.0
<a href="#">gi 3643902 gb AF086794.1 AF086794</a>	Plasmodium falciparum strai...	706	0.0
<a href="#">gi 160367 gb M28266.1 PFALIVANT</a>	Plasmodium falciparum liver-stag	287	5e-74

#### Alignments

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> [gi|510185|emb|Z30319.1|PFLSA15](#) P.falciparum LSA-1 gene for liver stage antigen-1 (5')  
Length=988

Score = 1729 bits (936), Expect = 0.0  
Identities = 954/954 (100%), Gaps = 0/954 (0%)  
Strand=Plus/Plus

Query	1	ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTGATATTTTCAT	60
Sbjct	33	.....	92
Query	61	ATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCATAAAATCTAACTTGAGA	120
Sbjct	93	.....	152
Query	121	AGTGGTTCTTCAAATTCTAGGAATCGAATAAATGAGGAAAATCACGAGAAGAAACACGTT	180
Sbjct	153	.....	212
Query	181	TTATCTCATAATTCATATGAGAAAATAAAATAATGAAAATAATAAATTTTTCGATAAG	240
Sbjct	213	.....	272
Query	241	GATAAAGAGTTAACGATGTCTAATGTAAAAAATGTGTACAAACAAATTTCAAAGTCTT	300
Sbjct	273	.....	332
Query	301	TTAAGAAATCTTGGTGTTTCAGAGAATATATTCCTTAAAGAAAATAAATTAAATAAGGAA	360
Sbjct	333	.....	392
Query	361	GGGAAATTAATTGAACACATAATAAATGATGATGACGATaaaaaaaaTATATTAAAGGG	420
Sbjct	393	.....	452
Query	421	CAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAGCAGCTAAAGAAAAGTTACAGGGG	480
Sbjct	453	.....	512
Query	481	CAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGC	540
Sbjct	513	.....	572
Query	541	GATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAA	600
Sbjct	573	.....	632

Query	601	CAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA	660
Sbjct	633	.....	692
Query	661	CTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAA	720
Sbjct	693	.....	752
Query	721	GAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTG	780
Sbjct	753	.....	812
Query	781	CAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAG	840
Sbjct	813	.....	872
Query	841	CAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGAT	900
Sbjct	873	.....	932
Query	901	TTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTA	954
Sbjct	933	.....	986

Score = 713 bits (386), Expect = 0.0  
Identities = 426/446 (95%), Gaps = 0/446 (0%)  
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	543	.....G..A.AA.....T.....T.....	602
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	603	.....G.....	662
Query	580	GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	663	.....T.....	722
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	723	.....G.....	782
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	783	.....	842
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	843	....T.....A.....G..G.....T.....	902
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	903	.....G.....A..A.....G....G.....G.	962
Query	880	TTGCAAGAACAACAAAGCGATTTAGA	905
Sbjct	963	.....	988

> [gi|9915|emb|X56203.1|PFLSA1G](#) P.falciparum LSA-1 gene for liver stage antigen  
Length=5970

Score = 1635 bits (885), Expect = 0.0  
Identities = 937/954 (98%), Gaps = 0/954 (0%)  
Strand=Plus/Plus

Query	1	ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTGATATTTTCA	60
Sbjct	79	.....	138
Query	61	ATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCATAAATCTAACTTGAGA	120
Sbjct	139	.....	198
Query	121	AGTGGTTCTTCAAATTCTAGGAATCGAATAAATGAGGAAAATCACGAGAAGAAACACGTT	180
Sbjct	199	.....G.....	258

Query	181	TTATCTCATAATTCATATGAGAAACTAAAAATAATGAAAATAATAAATTTTTTCGATAAG	240
Sbjct	259	.....	318
Query	241	GATAAAGAGTTAACGATGTCTAATGTAAAAAATGTGTACAAACAAATTTCAAAGTCTT	300
Sbjct	319	.....	378
Query	301	TTAAGAAATCTTGGTGTTCAGAGAATATATTCCTTAAAGAAAATAAATTAATAAGGAA	360
Sbjct	379	.....	438
Query	361	GGGAAATTAATTGAACACATAATAAATGATGATGACGATaaaaaaaaTATATTAAAGGG	420
Sbjct	439	.....	498
Query	421	CAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAGCAGCTAAAGAAAAGTTACAGGGG	480
Sbjct	499	.....C.....	558
Query	481	CAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGC	540
Sbjct	559	.....T.....T.....	618
Query	541	GATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAA	600
Sbjct	619	....C.....	678
Query	601	CAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA	660
Sbjct	679	.....T.....A.....G..G.....	738
Query	661	CTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAA	720
Sbjct	739	.....G..G.....	798
Query	721	GAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTG	780
Sbjct	799	.....	858
Query	781	CAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAG	840
Sbjct	859	.....G.....G.....A..A	918
Query	841	CAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGAT	900
Sbjct	919	.....G.....	978
Query	901	TTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	954
Sbjct	979	.....A.....	1032

Score = 848 bits (459), Expect = 0.0  
 Identities = 483/495 (97%), Gaps = 0/495 (0%)  
 Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	2476	.....A.A.....T.....	2535
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	2536	.....	2595
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	2596	.....	2655
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	2656	.....T.....A.....G.....	2715
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	2716	.....	2775
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	2776	.....	2835
Query	820	AAAGAAAAGTTACAAGAGCAGCAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	2836	.....G.....A.....A.....G....G.....	2895

Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA	939
Sbjct	2896	.....A.....	2955

Query	940	CAACAAAGCGATTTA	954
Sbjct	2956	.....	2970

Score = 843 bits (456), Expect = 0.0  
Identities = 482/495 (97%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	1201	.....G..A.AA.....T.....T....T.....	1260
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	1261	.....A.....G.....	1320
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	1321	.....	1380
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	1381	.....	1440
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	1441	.....	1500
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	1501	.....	1560
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	1561	.....G.....	1620
Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGGTTGCAAGAA	939
Sbjct	1621	.....C.....T.....A.....	1680
Query	940	CAACAAAGCGATTTA	954
Sbjct	1681	.....	1695

Score = 832 bits (450), Expect = 0.0  
Identities = 480/495 (96%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	3904	.....G..A.AA.....T.....	3963
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	3964	.....	4023
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	4024	.....T.....	4083
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	4084	.....G.....	4143
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	4144	.....T.....A.....	4203
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4204	.....T.....	4263
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4264	.....A.....A.....G....G.....	4323
Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGGTTGCAAGAA	939

Sbjct . 4324 . .....A..... 4383

Query 940 CAACAAAGCGATTTA 954  
Sbjct 4384 ..... 4398

Score = 832 bits (450), Expect = 0.0  
Identities = 480/495 (96%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query 460 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA 519  
Sbjct 4159 .....A.AA.....T..... 4218

Query 520 AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA 579  
Sbjct 4219 .....T.....A... 4278

Query 580 GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA 639  
Sbjct 4279 ..G.....A..... 4338

Query 640 AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA 699  
Sbjct 4339 .....G..... 4398

Query 700 GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG 759  
Sbjct 4399 ..... 4458

Query 760 AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT 819  
Sbjct 4459 ..... 4518

Query 820 AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG 879  
Sbjct 4519 .....G.....A.....A.....G.....G..... 4578

Query 880 TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA 939  
Sbjct 4579 .....A..... 4638

Query 940 CAACAAAGCGATTTA 954  
Sbjct 4639 ..... 4653

Score = 832 bits (450), Expect = 0.0  
Identities = 480/495 (96%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query 460 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA 519  
Sbjct 4312 .....G..A.AA.....T..... 4371

Query 520 AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA 579  
Sbjct 4372 .....G..... 4431

Query 580 GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA 639  
Sbjct 4432 ..... 4491

Query 640 AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA 699  
Sbjct 4492 .....G.....A..... 4551

Query 700 GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG 759  
Sbjct 4552 ..... 4611

Query 760 AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT 819  
Sbjct 4612 ..... 4671

Query 820 AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG 879  
Sbjct 4672 ..T.....G.....A.....A.....G.....G..... 4731

Query 880 TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA 939  
Sbjct 4732 .....A..... 4791



Query 940 CAACAAAGCGATTTA 954  
Sbjct 4792 ..... 4806

Score = 822 bits (445), Expect = 0.0  
Identities = 479/496 (96%), Gaps = 0/496 (0%)  
Strand=Plus/Plus

Query 459 AGCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGA 518  
Sbjct 3801 .....G.....A.A.....T..... 3860

Query 519 AAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCA 578  
Sbjct 3861 .....C...G..... 3920

Query 579 AGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACA 638  
Sbjct 3921 ..... 3980

Query 639 AAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTT 698  
Sbjct 3981 ..... 4040

Query 699 AGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGA 758  
Sbjct 4041 .....T..... 4100

Query 759 GAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGC 818  
Sbjct 4101 ..... 4160

Query 819 TAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAA 878  
Sbjct 4161 .....A..A.....G...G..... 4220

Query 879 GTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGA 938  
Sbjct 4221 .....T....T.....A...A..... 4280

Query 939 ACAACAAAGCGATTTA 954  
Sbjct 4281 G.....A..... 4296

Score = 821 bits (444), Expect = 0.0  
Identities = 476/492 (96%), Gaps = 0/492 (0%)  
Strand=Plus/Plus

Query 460 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA 519  
Sbjct 1354 .....G..A.AA.....T.....T..... 1413

Query 520 AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA 579  
Sbjct 1414 .....G..... 1473

Query 580 GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA 639  
Sbjct 1474 ..... 1533

Query 640 AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA 699  
Sbjct 1534 .....A.....G..G..... 1593

Query 700 GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG 759  
Sbjct 1594 .....T.....C..... 1653

Query 760 AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT 819  
Sbjct 1654 ....T..... 1713

Query 820 AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG 879  
Sbjct 1714 .....G..... 1773

Query 880 TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA 939  
Sbjct 1774 .....T.....A..... 1833

Query 940 CAACAAAGCGAT 951  
Sbjct 1834 ..... 1845

Score = 815 bits (441), Expect = 0.0  
Identities = 477/495 (96%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	3853	.....G..A.AA.....T.....C.....	3912
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	3913	.....G.....	3972
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	3973	.....T.....	4032
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTA	699
Sbjct	4033	.....	4092
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAG	759
Sbjct	4093	.....	4152
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4153	....T.....A.....G....	4212
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4213	.....G.....A..A.....	4272
Query	880	TTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA	939
Sbjct	4273	..A.....G.....A.....A.....	4332
Query	940	CAACAAAGCGATTTA 954	
Sbjct	4333	..... 4347	

Score = 815 bits (441), Expect = 0.0  
Identities = 477/495 (96%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	4261	.....A.A.....A....T.....	4320
Query	520	AAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	4321	.....G.....	4380
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	4381	.....	4440
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTA	699
Sbjct	4441	.....G.....	4500
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAG	759
Sbjct	4501	.....T.....G.....A.....	4560
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4561	.....G....	4620
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4621	.....G.....A..A.....G.....T.....	4680
Query	880	TTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA	939
Sbjct	4681	.....G.....A.....A.....	4740
Query	940	CAACAAAGCGATTTA 954	

Sbjct 4741 ..... 4755

Score = 809 bits (438), Expect = 0.0  
Identities = 476/495 (96%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	2119	.....G..A.AA.....T.....	2178
Query	520	AAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	2179	.....G.....	2238
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	2239	..G.....C.....	2298
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTA	699
Sbjct	2299	.....G.....	2358
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAG	759
Sbjct	2359	.....T....T.....A.....G.....	2418
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	2419	.....T.....	2478
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	2479	.....A.....G....G.....	2538
Query	880	TTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA	939
Sbjct	2539	.....T.....A.....	2598
Query	940	CAACAAAGCGATTTA	954
Sbjct	2599	.....	2613

Score = 809 bits (438), Expect = 0.0  
Identities = 476/495 (96%), Gaps = 0/495 (0%)  
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	2272	.....G..A.AA.....T.....	2331
Query	520	AAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	2332	.....T.....A...	2391
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	2392	..G.....	2451
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTA	699
Sbjct	2452	.....T.....A.....G.....	2511
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAG	759
Sbjct	2512	.....	2571
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	2572	....T.....G....	2631
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	2632	.....G.....A..A.....	2691
Query	880	TTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA	939
Sbjct	2692	..A.....G.....A.....	2751
Query	940	CAACAAAGCGATTTA	954
Sbjct	2752	.....	2766

Score = 809 bits (438), Expect = 0.0  
 Identities = 476/495 (96%), Gaps = 0/495 (0%)  
 Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAAGAGAGACGTGCTAAAGAA	519
Sbjct	3955	.....G..A.AA.....T.....T.....	4014
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	4015	.....	4074
Query	580	GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	4075	.....	4134
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	4135	.....A.....	4194
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	4195	.....T	4254
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4255	....T.....A.....G.....A.....G....	4314
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4315	.....G.....A..A.....G....G.....	4374
Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA	939
Sbjct	4375	.....A.....	4434
Query	940	CAACAAAGCGATTTA	954
Sbjct	4435	.....	4449

Score = 808 bits (437), Expect = 0.0  
 Identities = 490/515 (95%), Gaps = 5/515 (0%)  
 Strand=Plus/Plus

Query	442	GATCTTGAAGAA-AAAG-C-AGCTAAAGAAAAGTTACAGGGGCAACAAAGCGAT-TCAGA	497
Sbjct	1129	.....A...C..G.G..A.T.....C.-...	1187
Query	498	ACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAG	557
Sbjct	1188	.....T.....T..	1247
Query	558	ACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAA	617
Sbjct	1248	.....A.....G.....T.....	1307
Query	618	AGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTT	677
Sbjct	1308	.....G.....	1367
Query	678	GCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACA	737
Sbjct	1368	.....T.....	1427
Query	738	ACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGA	797
Sbjct	1428	.....	1487
Query	798	TTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACA	857
Sbjct	1488	.....G.....G.....A..A.....	1547
Query	858	AGATAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACG	917
Sbjct	1548	...G.....A.....G..G.....T	1607
Query	918	TGCTAAAGAAAGGTTGCAAGAACAACAAAGCGATT	952
Sbjct	1608	.....A.....	1642

**BLASTX 2.2.14 [May-07-2006]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1158786675-8897-80331541551.BLASTQ4

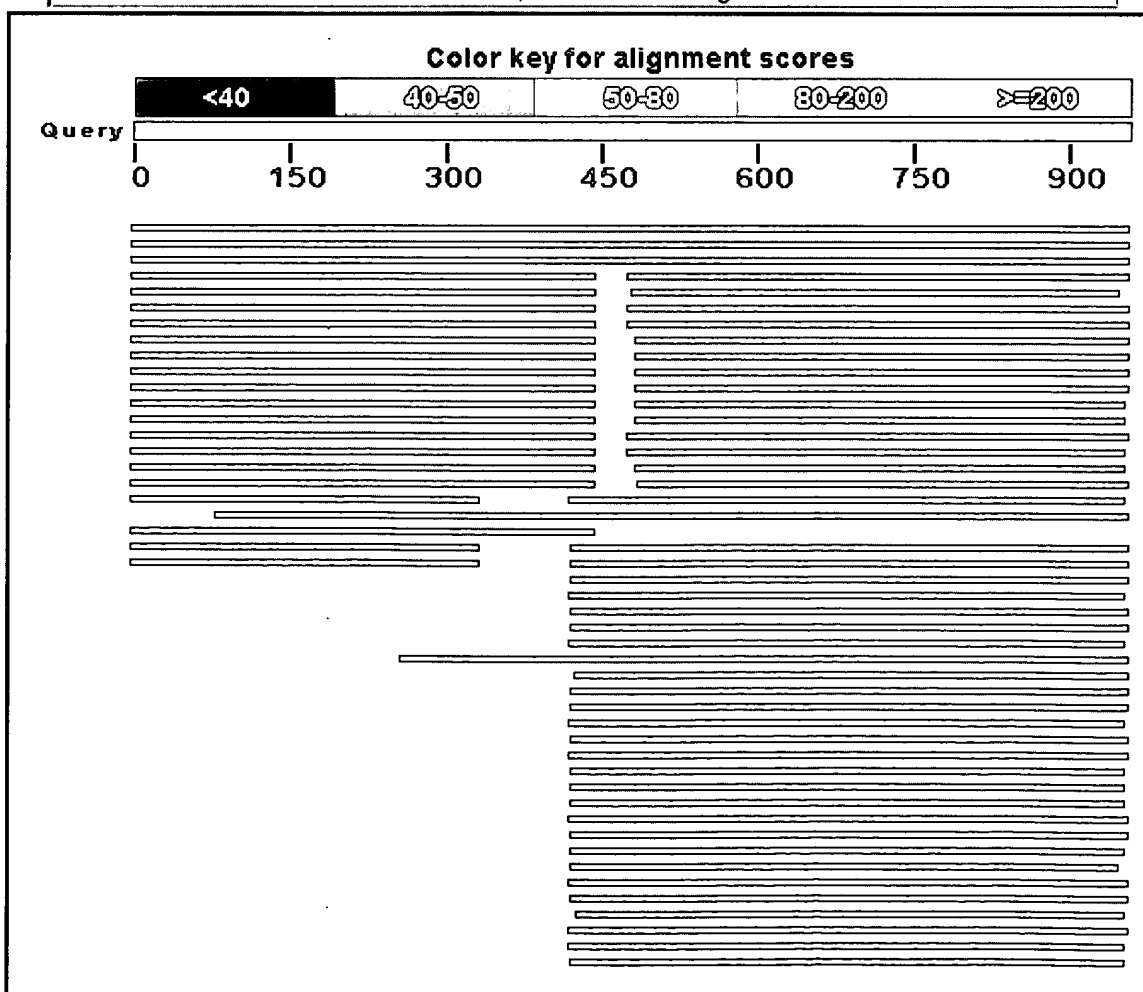
**Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
4,002,069 sequences; 1,381,387,148 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

Query= *SEQ ID NO: 38 vs protein database*  
Length=954

## Distribution of 1417 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments





Sequences producing significant alignments:

	Score (Bits)	E Value	
<a href="#">gi 510186 emb CAA82974.1 </a> liver stage antigen-1 [Plasmodium falc	441	2e-122	
<a href="#">gi 9916 emb CAA39663.1 </a> liver stage antigen [Plasmodium falcipar	426	6e-118	
<a href="#">gi 23508159 ref NP_700829.1 </a> liver stage antigen, putative [P...	402	9e-111	<b>G</b>
<a href="#">gi 510184 emb CAA82975.1 </a> liver stage antigen-1 [Plasmodium falc	284	4e-75	
<a href="#">gi 725322 gb AAC41594.1 </a> liver stage-specific antigen 1	149	2e-34	
<a href="#">gi 725300 gb AAC41583.1 </a> liver stage-specific antigen 1	149	2e-34	
<a href="#">gi 725320 gb AAC41593.1 </a> liver stage-specific antigen 1	147	5e-34	
<a href="#">gi 725302 gb AAC41584.1 </a> liver stage-specific antigen 1	147	5e-34	
<a href="#">gi 725306 gb AAC41586.1 </a> liver stage-specific antigen 1	147	7e-34	
<a href="#">gi 725310 gb AAC41588.1 </a> liver stage-specific antigen 1	147	7e-34	
<a href="#">gi 725304 gb AAC41585.1 </a> liver stage-specific antigen 1	147	7e-34	
<a href="#">gi 725312 gb AAC41589.1 </a> liver stage-specific antigen 1	147	9e-34	
<a href="#">gi 1435205 gb AAB04062.1 </a> liver stage antigen-1	146	1e-33	
<a href="#">gi 725326 gb AAC41596.1 </a> liver stage-specific antigen 1	145	2e-33	
<a href="#">gi 725324 gb AAC41595.1 </a> liver stage-specific antigen 1	145	3e-33	
<a href="#">gi 725308 gb AAC41587.1 </a> liver stage-specific antigen 1	144	8e-33	
<a href="#">gi 725314 gb AAC41590.1 </a> liver stage-specific antigen 1	142	2e-32	
<a href="#">gi 725316 gb AAC41591.1 </a> liver stage-specific antigen 1	142	2e-32	
<a href="#">gi 3643901 gb AAC42977.1 </a> liver stage-specific antigen-1 [Pla...	140	7e-32	
<a href="#">gi 58429870 gb AAW78331.1 </a> LSA-NRC [synthetic construct]	140	1e-31	
<a href="#">gi 725292 gb AAC41581.1 </a> liver stage-specific antigen 1	140	1e-31	
<a href="#">gi 3643903 gb AAC42978.1 </a> liver stage-specific antigen-1 [Pla...	139	2e-31	
<a href="#">gi 3643919 gb AAC42986.1 </a> liver stage-specific antigen-1 [Plasmo	137	6e-31	
<a href="#">gi 82705890 ref XP_727156.1 </a> hypothetical protein PY06496 [Pl...	122	3e-26	<b>G</b>
<a href="#">gi 225719 prf  1311343A</a> antigen, liver stage specific	117	1e-24	
<a href="#">gi 109509645 ref XP_001066623.1 </a> PREDICTED: hypothetical protein	115	4e-24	<b>G</b>
<a href="#">gi 109465334 ref XP_001075528.1 </a> PREDICTED: hypothetical protein	112	3e-23	<b>G</b>
<a href="#">gi 66803152 ref XP_635419.1 </a> hypothetical protein DDBDRAFT_01...	111	4e-23	<b>G</b>
<a href="#">gi 109467281 ref XP_001065891.1 </a> PREDICTED: hypothetical protein	110	1e-22	<b>G</b>
<a href="#">gi 84998962 ref XP_954202.1 </a> hypothetical protein TA20215 [Th...	109	2e-22	<b>G</b>
<a href="#">gi 109476246 ref XP_001061184.1 </a> PREDICTED: hypothetical protein	108	3e-22	<b>G</b>
<a href="#">gi 109510232 ref XP_001063700.1 </a> PREDICTED: similar to Cell d...	108	5e-22	<b>G</b>
<a href="#">gi 109509437 ref XP_001077753.1 </a> PREDICTED: hypothetical protein	108	5e-22	<b>G</b>
<a href="#">gi 109472296 ref XP_001060556.1 </a> PREDICTED: hypothetical protein	108	5e-22	<b>G</b>
<a href="#">gi 58429871 gb AAW78332.1 </a> truncated LSA-NRC [synthetic construc	105	2e-21	
<a href="#">gi 66800837 ref XP_629344.1 </a> SNF2-related domain-containing p...	105	2e-21	<b>G</b>
<a href="#">gi 109503258 ref XP_001072188.1 </a> PREDICTED: hypothetical protein	105	4e-21	<b>G</b>
<a href="#">gi 68356608 ref XP_696335.1 </a> PREDICTED: similar to Apoptotic ...	105	4e-21	<b>G</b>
<a href="#">gi 67479985 ref XP_655365.1 </a> villidin [Entamoeba histolytica ...	105	4e-21	<b>G</b>
<a href="#">gi 109509610 ref XP_001063252.1 </a> PREDICTED: hypothetical protein	104	5e-21	<b>G</b>
<a href="#">gi 109506221 ref XP_001073883.1 </a> PREDICTED: hypothetical protein	104	5e-21	<b>G</b>
<a href="#">gi 109480113 ref XP_001063529.1 </a> PREDICTED: hypothetical protein	103	9e-21	<b>G</b>
<a href="#">gi 68356430 ref XP_687786.1 </a> PREDICTED: similar to Apoptotic ...	103	2e-20	<b>G</b>
<a href="#">gi 109509374 ref XP_001076719.1 </a> PREDICTED: hypothetical protein	102	3e-20	<b>G</b>
<a href="#">gi 66802666 ref XP_635205.1 </a> hypothetical protein DDBDRAFT_01...	102	3e-20	<b>G</b>
<a href="#">gi 66813268 ref XP_640813.1 </a> SAP DNA-binding domain-containin...	102	3e-20	<b>G</b>
<a href="#">gi 5669894 gb AAD46501.1 AF148805_6</a> ORF73 [Human herpesvirus 8]	101	4e-20	

<a href="#">gi 11037008 gb AAG27458.1 AF305694.1</a>	latent nuclear antigen [Hum	<a href="#">101</a>	4e-20	
<a href="#">gi 109497810 ref XP_001058181.1 </a>	PREDICTED: hypothetical protein	<a href="#">101</a>	6e-20	<b>G</b>
<a href="#">gi 109487363 ref XP_001058747.1 </a>	PREDICTED: hypothetical protein	<a href="#">100</a>	8e-20	<b>G</b>
<a href="#">gi 109469884 ref XP_001063460.1 </a>	PREDICTED: hypothetical protein	<a href="#">100</a>	1e-19	<b>G</b>
<a href="#">gi 9886896 gb AAG01636.1 </a>	Orf73 [Human herpesvirus 8]	<a href="#">100</a>	1e-19	
<a href="#">gi 66810592 ref XP_639003.1 </a>	hypothetical protein DDBDRAFT_01...	<a href="#">100</a>	1e-19	<b>G</b>
<a href="#">gi 13936996 gb AAK50002.1 </a>	ORF73 [Human herpesvirus 8]	<a href="#">99.8</a>	2e-19	
<a href="#">gi 109464413 ref XP_001071056.1 </a>	PREDICTED: hypothetical protein	<a href="#">99.4</a>	2e-19	<b>G</b>
<a href="#">gi 94407897 ref XP_979552.1 </a>	PREDICTED: hypothetical protein [Mu	<a href="#">99.4</a>	2e-19	<b>G</b>
<a href="#">gi 2246532 gb AAB62657.1 </a>	ORF 73 [Human herpesvirus 8]	<a href="#">99.4</a>	2e-19	
<a href="#">gi 37725922 gb AAO38039.1 </a>	reticulocyte binding-like protein 2b	<a href="#">99.0</a>	3e-19	
<a href="#">gi 18846043 ref NP_572129.1 </a>	ORF 73; extensive acidic domains...	<a href="#">99.0</a>	3e-19	<b>G</b>
<a href="#">gi 66808553 ref XP_637999.1 </a>	LIM domain-containing protein [D...	<a href="#">99.0</a>	3e-19	<b>G</b>
<a href="#">gi 67477997 ref XP_654429.1 </a>	Grainin 2 [Entamoeba histolytica...	<a href="#">98.6</a>	4e-19	<b>G</b>
<a href="#">gi 28829643 gb AAO52159.1 </a>	similar to C25A11.4b.p [Caenorhabd...	<a href="#">98.2</a>	5e-19	
<a href="#">gi 66819811 ref XP_643564.1 </a>	fimbrin-related RasGAP protein [...	<a href="#">98.2</a>	5e-19	<b>G</b>
<a href="#">gi 111306569 gb AAI21747.1 </a>	Unknown (protein for IMAGE:8158662)	<a href="#">97.8</a>	6e-19	<b>G</b>
<a href="#">gi 92096287 gb AAI15075.1 </a>	Unknown (protein for IMAGE:7448149) [	<a href="#">97.8</a>	6e-19	<b>U G</b>
<a href="#">gi 89286901 gb EAR84895.1 </a>	hypothetical protein THERM_005845...	<a href="#">97.1</a>	1e-18	
<a href="#">gi 38566922 emb CAE76225.1 </a>	related to putative cytoplasmic s...	<a href="#">96.7</a>	1e-18	
<a href="#">gi 85111555 ref XP_963992.1 </a>	hypothetical protein [Neurospora...	<a href="#">96.7</a>	1e-18	<b>G</b>
<a href="#">gi 66815949 ref XP_641991.1 </a>	hypothetical protein DDBDRAFT_02...	<a href="#">96.3</a>	2e-18	<b>G</b>
<a href="#">gi 109480597 ref XP_001053178.1 </a>	PREDICTED: hypothetical protein	<a href="#">95.9</a>	2e-18	<b>G</b>
<a href="#">gi 73981602 ref XP_540325.2 </a>	PREDICTED: similar to Trichohyalin	<a href="#">95.9</a>	2e-18	<b>G</b>
<a href="#">gi 66806319 ref XP_636882.1 </a>	hypothetical protein DDBDRAFT_01...	<a href="#">95.9</a>	2e-18	<b>G</b>
<a href="#">gi 82594248 ref XP_725343.1 </a>	hypothetical protein PY04960 [Pl...	<a href="#">95.1</a>	4e-18	<b>G</b>
<a href="#">gi 113420216 ref XP_001130141.1 </a>	PREDICTED: hypothetical protein	<a href="#">94.4</a>	7e-18	<b>G</b>
<a href="#">gi 56409774 emb CAF25315.1 </a>	NBP2b protein [Plasmodium falciparum	<a href="#">94.4</a>	7e-18	
<a href="#">gi 23508608 ref NP_701277.1 </a>	hypothetical protein PF11_0418 [...	<a href="#">94.4</a>	7e-18	<b>E G</b>
<a href="#">gi 66816387 ref XP_642203.1 </a>	hypothetical protein DDB_0214889...	<a href="#">94.4</a>	7e-18	<b>G</b>
<a href="#">gi 7549210 gb AAF63787.1 AF142406.1</a>	200 kDa antigen p200 [Babesi	<a href="#">94.0</a>	9e-18	
<a href="#">gi 73958144 ref XP_546992.2 </a>	PREDICTED: similar to Zinc finge...	<a href="#">94.0</a>	9e-18	<b>G</b>
<a href="#">gi 24580684 ref NP_608540.1 </a>	CG2839-PA [Drosophila melanogast...	<a href="#">94.0</a>	9e-18	<b>U G</b>
<a href="#">gi 67466733 ref XP_649508.1 </a>	conserved hypothetical protein [...	<a href="#">94.0</a>	9e-18	<b>G</b>
<a href="#">gi 94386777 ref XP_928149.2 </a>	PREDICTED: hypothetical protein [Mu	<a href="#">93.6</a>	1e-17	<b>G</b>
<a href="#">gi 23619293 ref NP_705255.1 </a>	reticulocyte binding protein 2 h...	<a href="#">93.2</a>	2e-17	<b>E G</b>
<a href="#">gi 13345187 gb AAK19244.1 AF312916.1</a>	reticulocyte binding pro...	<a href="#">93.2</a>	2e-17	
<a href="#">gi 437639 gb AAA72295.1 </a>	[Plasmodium falciparum 3' end.], gene p	<a href="#">93.2</a>	2e-17	
<a href="#">gi 23613070 ref NP_703392.1 </a>	hypothetical protein [Plasmodium...	<a href="#">92.8</a>	2e-17	<b>E G</b>
<a href="#">gi 66804281 ref XP_635920.1 </a>	hypothetical protein DDBDRAFT_01...	<a href="#">92.4</a>	3e-17	<b>G</b>
<a href="#">gi 109500521 ref XP_001075353.1 </a>	PREDICTED: hypothetical protein	<a href="#">92.0</a>	4e-17	<b>G</b>
<a href="#">gi 61353791 gb AAX44045.1 </a>	clock [Macrobrachium rosenbergii]	<a href="#">92.0</a>	4e-17	
<a href="#">gi 71548239 ref ZP_00668622.1 </a>	similar to Chromosome segregat...	<a href="#">92.0</a>	4e-17	
<a href="#">gi 66813088 ref XP_640723.1 </a>	hypothetical protein DDBDRAFT_02...	<a href="#">91.7</a>	5e-17	<b>G</b>
<a href="#">gi 109461086 ref XP_001068158.1 </a>	PREDICTED: hypothetical protein	<a href="#">91.3</a>	6e-17	<b>G</b>
<a href="#">gi 11493973 gb AAG35726.1 AF208229.1</a>	lipase precursor GehM [Stap	<a href="#">91.3</a>	6e-17	
<a href="#">gi 85104285 ref XP_961717.1 </a>	hypothetical protein [Neurospora...	<a href="#">90.9</a>	8e-17	<b>G</b>
<a href="#">gi 109493310 ref XP_001067694.1 </a>	PREDICTED: similar to 60S ri...	<a href="#">90.5</a>	1e-16	<b>G</b>
<a href="#">gi 109490763 ref XP_001075128.1 </a>	PREDICTED: hypothetical protein	<a href="#">90.5</a>	1e-16	<b>G</b>
<a href="#">gi 109501038 ref XP_001057439.1 </a>	PREDICTED: hypothetical protein	<a href="#">89.7</a>	2e-16	<b>G</b>
<a href="#">gi 109472820 ref XP_001076490.1 </a>	PREDICTED: hypothetical protein	<a href="#">89.7</a>	2e-16	<b>G</b>
<a href="#">gi 94396405 ref XP_984315.1 </a>	PREDICTED: hypothetical protein [Mu	<a href="#">89.7</a>	2e-16	<b>G</b>
<a href="#">gi 467292 gb AAA17387.1 </a>	glutamine-asparagine rich protein	<a href="#">89.7</a>	2e-16	

## Alignments

Get selected sequences

Select all

Deselect all

> gi|510186|emb|CAA82974.1| liver stage antigen-1 [Plasmodium falciparum]  
Length=318

Score = 441 bits (1135), Expect = 2e-122

Identities = 318/318 (100%), Positives = 318/318 (100%), Gaps = 0/318 (0%)

Frame = +1

Query	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKsnlrsqssnsrnrineenheKKHV	180
		MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEENHEKKHV	
Sbjct	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEENHEKKHV	60
Query	181	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	360
		LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	
Sbjct	61	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	120
Query	361	gkliehiinddddKKKYIKGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	540
		GKLIEHIINDDDDKKKYIKGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	
Sbjct	121	GKLIEHIINDDDDKKKYIKGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	180
Query	541	DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	720
		DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	
Sbjct	181	DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	240
Query	721	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	900
		EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	
Sbjct	241	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	300
Query	901	LEQERRAKERLQEQQSDL	954
		LEQERRAKERLQEQQSDL	
Sbjct	301	LEQERRAKERLQEQQSDL	318

> gi|9916|emb|CAA39663.1| liver stage antigen [Plasmodium falciparum]  
Length=1909

Score = 426 bits (1096), Expect = 6e-118

Identities = 309/318 (97%), Positives = 311/318 (97%), Gaps = 0/318 (0%)

Frame = +1

Query	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKsnlrsqssnsrnrineenheKKHV	180
		MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEE HEKKHV	
Sbjct	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEEHEKKHV	60
Query	181	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	360
		LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	
Sbjct	61	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	120
Query	361	gkliehiinddddKKKYIKGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	540
		GKLIEHIINDDDDKKKYIKGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	
Sbjct	121	GKLIEHIINDDDDKKKYIKGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	180
Query	541	DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	720
		DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	
Sbjct	181	DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	240
Query	721	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	900
		EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	
Sbjct	241	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSD	300



Query 901 LEQERRAKERLQEQQSDL 954  
LEQERRAKE+LQEQQSDL  
Sbjct 301 LEQERRAKEKLQEQQSDL 318

Score = 287 bits (735), Expect = 4e-76  
Identities = 153/160 (95%), Positives = 156/160 (97%), Gaps = 0/160 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
Sbjct 805 QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 864

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ  
Sbjct 865 DRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 924

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL  
Sbjct 925 EQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 964

Score = 287 bits (734), Expect = 6e-76  
Identities = 153/160 (95%), Positives = 156/160 (97%), Gaps = 0/160 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
Sbjct 737 QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 796

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ  
Sbjct 797 DRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ 856

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
EQQSDLEQDRLAKEKLQEQQSDLEQERRAKE+LQEQQSDL  
Sbjct 857 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 896

Score = 284 bits (726), Expect = 5e-75  
Identities = 152/160 (95%), Positives = 155/160 (96%), Gaps = 0/160 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
Q QQSD EQ+R AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
Sbjct 380 QEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 439

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ  
Sbjct 440 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 499

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
EQQSDLEQ+RLAKEKLQEQQSD EQER AKE+LQEQQSDL  
Sbjct 500 EQQSDLEQERLAKEKLQEQQSDSEQERLAKEKLQEQQSDL 539

Score = 283 bits (725), Expect = 6e-75  
Identities = 153/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
Sbjct 261 QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 320

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834

Sbjct 321 ERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ QQSDLEQERLAKEKLQ 380  
 ERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDLEQERLAKEKLQ

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQDRLAKEKLQEQQSDLEQER AKE+LQEQQSDL

Sbjct 381 EQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 420

Score = 283 bits (724), Expect = 8e-75  
 Identities = 151/160 (94%), Positives = 155/160 (96%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ

Sbjct 703 QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 762

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 +RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQ

Sbjct 763 DRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQ 822

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL

Sbjct 823 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 862

Score = 283 bits (724), Expect = 8e-75  
 Identities = 151/160 (94%), Positives = 154/160 (96%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQ

Sbjct 1366 QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 1425

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ

Sbjct 1426 ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 1485

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL

Sbjct 1486 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1525

Score = 283 bits (723), Expect = 1e-74  
 Identities = 152/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ

Sbjct 1196 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 1255

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ

Sbjct 1256 ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 1315

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL

Sbjct 1316 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1355

Score = 283 bits (723), Expect = 1e-74  
 Identities = 152/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ

Sbjct	1213	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1272
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERLAKEKLQ	834
Sbjct	1273	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQ	1332
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	1333	EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDL 1372	

Score = 282 bits (722), Expect = 1e-74  
Identities = 152/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
Sbjct	227	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	286
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERLAKEKLQ	834
Sbjct	287	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQ	346
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLAKEKLQ QQSDLEQER AKE+LQEQQSDL	
Sbjct	347	EQQSDLEQERLAKEKLQGQQSDLEQERLAKEKLQEQQSDL 386	

Score = 282 bits (722), Expect = 1e-74  
Identities = 152/160 (95%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ	654
Sbjct	1264	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ	1323
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	1324	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ	1383
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQDRLAKEKLQEQQ DLEQERRAKE+LQEQQSDL	
Sbjct	1384	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1423	

Score = 282 bits (722), Expect = 1e-74  
Identities = 151/160 (94%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
Sbjct	1417	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1476
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLA EKLQ	834
Sbjct	1477	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLANEKLQ	1536
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	1537	EQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1576	

Score = 281 bits (718), Expect = 4e-74  
Identities = 151/160 (94%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	669	QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	728
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQ	
Sbjct	729	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQ	788
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQDRLAKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	789	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL	828

Score = 280 bits (717), Expect = 5e-74  
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	1332	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1391
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		+RLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ	
Sbjct	1392	DRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	1451
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQ DL	
Sbjct	1452	EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDL	1491

Score = 280 bits (716), Expect = 7e-74  
Identities = 151/160 (94%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	414	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	473
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSD EQERLAKEKLQ	
Sbjct	474	ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDSEQERLAKEKLQ	533
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	534	EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL	573

Score = 280 bits (715), Expect = 9e-74  
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	839	QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	898
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQER AKEKLQEQQ DLEQERRAKEKLQEQQSDLEQER AKEKLQ	
Sbjct	899	ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	958
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	959	EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL	998

Score = 280 bits (715), Expect = 9e-74  
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	1247	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1306
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	
Sbjct	1307	ERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	1366
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQSDLEQ+R AKEKLQEQQSDLEQ+R AKE+LQEQQ DL	
Sbjct	1367	EQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQRDL 1406	

Score = 280 bits (715), Expect = 9e-74  
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQ	
Sbjct	1281	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ	1340
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+RLAKEKLQ	
Sbjct	1341	ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQ	1400
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	1401	EQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1440	

Score = 280 bits (715), Expect = 9e-74  
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQER AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	1298	QEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1357
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQ DLEQER AKEKLQ	
Sbjct	1358	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQRDLEQERRAKEKLQ	1417
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQSDLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	1418	EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1457	

Score = 279 bits (714), Expect = 1e-73  
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQ+R AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	856	QEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	915
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ERLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	
Sbjct	916	ERLAKEKLQEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	975
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQ QQSDL	

Sbjct 976 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDL 1015

Score = 278 bits (712), Expect = 2e-73  
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
Q QQSD EQER AKEKLQEQQSDLEQERLAKEKLQ QQSDLEQER AKEKLQEQQSDLEQ  
Sbjct 329 QEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDLEQERLAKEKLQEQQSDLEQ 388  
Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
+RLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ  
Sbjct 389 DRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 448  
Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
EQQSDLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL  
Sbjct 449 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 488

Score = 278 bits (712), Expect = 2e-73  
Identities = 149/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
Sbjct 771 QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 830  
Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQ  
Sbjct 831 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQ 890  
Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQ DL  
Sbjct 891 EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQRDL 930

Score = 278 bits (711), Expect = 3e-73  
Identities = 149/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
Sbjct 686 QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 745  
Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
ER AKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+RLAKEKLQ  
Sbjct 746 ERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQ 805  
Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQSDL  
Sbjct 806 EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDL 845

Score = 278 bits (710), Expect = 3e-73  
Identities = 149/159 (93%), Positives = 152/159 (95%), Gaps = 0/159 (0%)  
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
QGQQSD EQER AKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQ  
Sbjct 363 QGQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 422  
Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ  
Sbjct 423 ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 482

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSD 951  
 EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSD  
 Sbjct 483 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSD 521

Score = 278 bits (710), Expect = 3e-73  
 Identities = 148/160 (92%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 QGQQSD EQER AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLE+  
 Sbjct 1128 QGQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLER 1187

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 + +KE LQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ  
 Sbjct 1188 TKASKETLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 1247

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL  
 Sbjct 1248 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1287

Score = 278 bits (710), Expect = 3e-73  
 Identities = 150/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
 Sbjct 1230 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 1289

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ  
 Sbjct 1290 ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ 1349

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL  
 Sbjct 1350 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1389

Score = 277 bits (709), Expect = 5e-73  
 Identities = 150/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
 Sbjct 431 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 490

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 ERLAKEKLQEQQSDLEQER AKEKLQEQQSD EQER AKEKLQEQQSDLEQERLAKEKLQ  
 Sbjct 491 ERLAKEKLQEQQSDLEQERLAKEKLQEQQSDSEQERLAKEKLQEQQSDLEQERLAKEKLQ 550

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL  
 Sbjct 551 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 590

Score = 277 bits (708), Expect = 6e-73  
 Identities = 148/160 (92%), Positives = 153/160 (95%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD E+ + +KE LQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ  
 Sbjct 1179 QEQQSDLERTKASKETLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 1238

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ  
 Sbjct 1239 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 1298

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL  
 Sbjct 1299 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 1338

Score = 276 bits (707), Expect = 8e-73  
 Identities = 154/177 (87%), Positives = 155/177 (87%), Gaps = 17/177 (9%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEK-----LQEQQSDLEQ 603  
 QGQQSD EQER AKEKLQEQQSDLEQERLAKEK LQEQQSDLEQ  
 Sbjct 618 QGQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLERTKASKETLQEQQSDLEQ 677

Query 604 ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 783  
 ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ  
 Sbjct 678 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 737

Query 784 EQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQER AKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKE+LQEQQSDL  
 Sbjct 738 EQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 794

Score = 276 bits (705), Expect = 1e-72  
 Identities = 149/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ  
 Sbjct 278 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 337

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 ERLAKEKLQEQQSDLEQER AKEKLQ QQSDLEQER AKEKLQEQQSDLEQ+RLAKEKLQ  
 Sbjct 338 ERLAKEKLQEQQSDLEQERLAKEKLQGGQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQ 397

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL  
 Sbjct 398 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 437

Score = 276 bits (705), Expect = 1e-72  
 Identities = 149/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654  
 Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQ  
 Sbjct 295 QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 354

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834  
 ERLAKEKLQ QQSDLEQER AKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQERLAKEKLQ  
 Sbjct 355 ERLAKEKLQGGQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQ 414

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954  
 EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQSDL  
 Sbjct 415 EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDL 454

Score = 276 bits (705), Expect = 1e-72  
 Identities = 149/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)  
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654



Sbjct	312	Q QQSD EQER AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQER AKEKLQ QQSDLEQ QEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDLEQ	371
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	372	ERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ	431
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	432	EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 471	

Score = 275 bits (704), Expect = 2e-72  
Identities = 148/160 (92%), Positives = 151/160 (94%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ+R AKEKLQEQQ DLEQ	654
Sbjct	1349	QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQRDLEQ	1408
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	1409	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	1468
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLAKEKLQEQQ DLEQERRAKE+LQEQQSDL	
Sbjct	1469	EQQSDLEQERLAKEKLQEQQRDLEQERRAKEKLQEQQSDL 1508	

Score = 275 bits (704), Expect = 2e-72  
Identities = 148/160 (92%), Positives = 150/160 (93%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQ D EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
Sbjct	1400	QEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1459
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQER AKEKLQEQQ DLEQERRAKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	1460	ERRAKEKLQEQQSDLEQERLAKEKLQEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	1519
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLA EKLQEQQ DLEQERRAKE+LQEQQSDL	
Sbjct	1520	EQQSDLEQERLANEKLQEQQRDLEQERRAKEKLQEQQSDL 1559	

Score = 275 bits (703), Expect = 2e-72  
Identities = 149/160 (93%), Positives = 151/160 (94%), Gaps = 0/160 (0%)  
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ	654
Sbjct	397	QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ	456
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERLAKEKLQ	834
Sbjct	457	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQ	516
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSD EQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	517	EQQSDSEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 556	

Score = 275 bits (703), Expect = 2e-72  
Identities = 149/160 (93%), Positives = 151/160 (94%), Gaps = 0/160 (0%)